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<141> 2000-08-02

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aatcaaataa	tgattttatt	ttgactgata	gtgacctgtt	cgttgcaaca	aattgataag	4860
caatgctttt	ttataatgcc	aacttagtat	aaaaaagctg	aacgagaaac	gtaaaatgat	4920
ataaatatca	atatattaaa	ttagattttg	cataaaaaac	agactacata	atactgtaaa	4980
acacaacata	tgcagtcact	atgaatcaac	tacttagatg	gtattagtga	cctgtaacag	5040
agcattagcg	caaggtgatt	tttgtcttct	tgcgctaatt	ttttgtcatc	aaacctgtcg	5100
catgatcatg	gggctgcagg	aattcgatgg	tcgaatttgc	tttcgaattt	ctgccattca	5160
tccgcttatt	atcacttatt	caggcgtagc	accaggcgtt	taagggcacc	aataactgcc	5220
ttaaaaaaat	tacgccccgc	cctgccactc	atcgcagtac	tgttgtaatt	cattaagcat	5280
tctgccgaca	tggaagccat	cacagacggc	atgatgaacc	tgaatcgcca	gcggcatcag	5340
cacettgtcg	ccttgcgat	aataatttgc	catggtgaaa	acgggggcga	agaagttgtc	5400
catattggcc	acgtttaaat	caaaactggg	gaaactcacc	cagggattgg	ctgagacgaa	5460
aaacatattc	tcaataaacc	ctttagggaa	ataggccagg	ttttcaccgt	aacacgccac	5520
atcttgcgaa	tatatgtgta	gaaactgccg	gaaatcgctg	tggatttcac	tccagagcga	5580
tgaaaacggt	tcagtttgct	catggaaaac	ggtgtaacaa	gggtgaacac	tatcccatat	5640
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<211> 238

<212> DNA

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<220>

<223> LacZ(/chitobiase Fusion

<220>

<221> CDS

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<221> -35_signal
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<221> -10_signal
<222> (69)...(74)
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<221> protein_bind
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ccggctcgta tgttggtgagc aattgtgagc ggataacaat ttcacacagg aaacagct 118
atg acc atg att acg cca agc ttg cat gcc tgc agg tcg act cta gag 166
Met Thr Met Ile Thr Pro Ser Leu His Ala Cys Arg Ser Thr Leu Glu
1 5 10 15

gat ccc cgg gta ccg agc tot gag caa caa gtt gta aac tca ctg gct 214
Asp Pro Arg Val Pro Ser Ser Glu Gln Gln Val Val Asn Ser Leu Ala
20 25 30

gat aac ctt gat atc caa tat gaa 238
Asp Asn Leu Asp Ile Gln Tyr Glu
35 40

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<212> PRT
<213> Artificial Sequence
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<223> LacZ(/chitobiase Fusion

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1 5 10 15
Asp Pro Arg Val Pro Ser Ser Glu Gln Gln Val Val Asn Ser Leu Ala
20 25 30
Asp Asn Leu Asp Ile Gln Tyr Glu
35 40

<210> 17
<211> 22
<212> PRT
<213> Artificial Sequence
<220>
<223> dnaA/chitobiase Fusion

<400> 17
Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu
1 5 10 15
Leu Val Pro Ser Ser Glu

<210> 18
 <211> 2643
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(2643)

<223> dnaA/Chitobiase Fusion

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 Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu
 1 5 10 15

ttg gta ccg agc tct gag caa caa gtt gta aac tca ctg gct gat aac 96
 Leu Val Pro Ser Ser Glu Gln Gln Val Val Asn Ser Leu Ala Asp Asn
 20 25 30

ctt gat atc caa tat gaa gtg tta act aac cat ggt gct aac gaa ggt 144
 Leu Asp Ile Gln Tyr Glu Val Leu Thr Asn His Gly Ala Asn Glu Gly
 35 40 45

ctt gcg tgc caa gat atg ggc gca gaa tgg gct tct tgt aac aaa gta 192
 Leu Ala Cys Gln Asp Met Gly Ala Glu Trp Ala Ser Cys Asn Lys Val
 50 55 60

aac atg acg ctt gtt aac caa ggt gaa gct gtt gac tca aaa gat tgg 240
 Asn Met Thr Leu Val Asn Gln Gly Glu Ala Val Asp Ser Lys Asp Trp
 65 70 75 80

gct att tac ttc cac agc att cgt ctg att ctg gat gtt gac aac gag 288
 Ala Ile Tyr Phe His Ser Ile Arg Leu Ile Leu Asp Val Asp Asn Glu
 85 90 95

cag ttc aaa atc tct cgt gta acg ggt gac cta cat aag cta gaa cca 336
 Gln Phe Lys Ile Ser Arg Val Thr Gly Asp Leu His Lys Leu Glu Pro
 100 105 110

aca gat aag ttt gac ggc ttc gct gcc ggt gaa gag gtt gtt ctt cca 384
 Thr Asp Lys Phe Asp Gly Phe Ala Ala Gly Glu Glu Val Val Leu Pro
 115 120 125

ttg gtt ggt gaa tac tgg caa cta ttt gaa act gac ttc atg ccg ggt 432
 Leu Val Gly Glu Tyr Trp Gln Leu Phe Glu Thr Asp Phe Met Pro Gly
 130 135 140

gca ttc gtt tct gct cca aac gca gaa cct aag atg att gct tct cta 480
 Ala Phe Val Ser Ala Pro Asn Ala Glu Pro Lys Met Ile Ala Ser Leu
 145 150 155 160

aat act gaa gat gtt gcg tct ttt gtg acg ggt ctt gaa ggt aac aac 528
 Asn Thr Glu Asp Val Ala Ser Phe Val Thr Gly Leu Glu Gly Asn Asn
 165 170 175

cta aaa cgt aca cca gat gac aac aat gta ttt gca aac gct gtg tct Leu Lys Arg Thr Pro Asp Asp Asn Asn Val Phe Ala Asn Ala Val Ser 180 185 190	576
cgt ttt gag aaa aac gaa gac cta gca aca caa gac gta tca acc acg Arg Phe Glu Lys Asn Glu Asp Leu Ala Thr Gln Asp Val Ser Thr Thr 195 200 205	624
tta cta cca aca cca atg cac gtt gaa gcg ggt aaa ggc aaa gta gat Leu Leu Pro Thr Pro Met His Val Glu Ala Gly Lys Gly Lys Val Asp 210 215 220	672
atc gcg gat ggt att gcg ctg cct aaa gac gca ttc gat gcg act cag Ile Ala Asp Gly Ile Ala Leu Pro Lys Asp Ala Phe Asp Ala Thr Gln 225 230 235 240	720
ttc gca gcg att caa gat cgt gca gaa gtg gta ggt gtg gac gtt cgt Phe Ala Ala Ile Gln Asp Arg Ala Glu Val Val Gly Val Asp Val Arg 245 250 255	768
ggc gat ctt cct gta agc atc act gtt gtt cct gca gac ttc acc ggt Gly Asp Leu Pro Val Ser Ile Thr Val Val Pro Ala Asp Phe Thr Gly 260 265 270	816
gaa tta gca aaa tct ggt gct tac gaa atg agc atc aaa ggc gac ggt Glu Leu Ala Lys Ser Gly Ala Tyr Glu Met Ser Ile Lys Gly Asp Gly 275 280 285	864
att gtg att aaa gcg ttc gac caa gca ggc gct ttc tac gca gta caa Ile Val Ile Lys Ala Phe Asp Gln Ala Gly Ala Phe Tyr Ala Val Gln 290 295 300	912
tct atc ttt ggc ctg gta gat agc caa aat gct gat tct cta cca caa Ser Ile Phe Gly Leu Val Asp Ser Gln Asn Ala Asp Ser Leu Pro Gln 305 310 315 320	960
ctg tct att aaa gat gcg cct cgt ttt gat tac cgt ggt gtg atg gtg Leu Ser Ile Lys Asp Ala Pro Arg Phe Asp Tyr Arg Gly Val Met Val 325 330 335	1008
gat gtg gct cgt aac ttc cac tct aag gac gca atc ctt gca acg cta Asp Val Ala Arg Asn Phe His Ser Lys Asp Ala Ile Leu Ala Thr Leu 340 345 350	1056
gac caa atg gca gcg tac aag atg aac aaa ctt cac ctt cac cta acc Asp Gln Met Ala Ala Tyr Lys Met Asn Lys Leu His Leu His Leu Thr 355 360 365	1104
gat gat gaa ggc tgg cgt tta gaa atc ccg ggt ctg cct gag ctg aca Asp Asp Glu Gly Trp Arg Leu Glu Ile Pro Gly Leu Pro Glu Leu Thr 370 375 380	1152
gaa gtg ggt gct aac cgt tgt ttc gat aca caa gag aaa agc tgt tta Glu Val Gly Ala Asn Arg Cys Phe Asp Thr Gln Glu Lys Ser Cys Leu 385 390 395 400	1200

ctg cct cag ctt ggc tct ggt cca acg aca gac aac ttt ggc tct ggc	1248
Leu Pro Gln Leu Gly Ser Gly Pro Thr Thr Asp Asn Phe Gly Ser Gly	
405 410 415	
tac ttc agc aaa gca gac tac gtg gaa atc ttg aaa tac gcg aaa gca	1296
Tyr Phe Ser Lys Ala Asp Tyr Val Glu Ile Leu Lys Tyr Ala Lys Ala	
420 425 430	
cgt aac att gaa gtg att cca gaa atc gat atg cca gct cac gct cgt	1344
Arg Asn Ile Glu Val Ile Pro Glu Ile Asp Met Pro Ala His Ala Arg	
435 440 445	
gca gca gta gta tca atg gaa gct cgt tac gac cgc cta atg gaa gaa	1392
Ala Ala Val Val Ser Met Glu Ala Arg Tyr Asp Arg Leu Met Glu Glu	
450 455 460	
ggg aaa gaa gct gaa gcg aac gaa tac cgt ctg atg gat cct caa gat	1440
Gly Lys Glu Ala Glu Ala Asn Glu Tyr Arg Leu Met Asp Pro Gln Asp	
465 470 475 480	
aca tca aac gta acg acg gtt cag ttc tac aat aag caa agc ttc atc	1488
Thr Ser Asn Val Thr Thr Val Gln Phe Tyr Asn Lys Gln Ser Phe Ile	
485 490 495	
aac cca tgt atg gaa tct tca act cgc ttt gtt gat aag gtg att tca	1536
Asn Pro Cys Met Glu Ser Ser Thr Arg Phe Val Asp Lys Val Ile Ser	
500 505 510	
gaa gtg gca gca atg cac caa gaa gct ggc gct cca cta aca act tgg	1584
Glu Val Ala Ala Met His Gln Glu Ala Gly Ala Pro Leu Thr Thr Trp	
515 520 525	
cac ttc ggt ggt gac gaa gcg aag aac atc aag cta ggt gct ggt ttc	1632
His Phe Gly Gly Asp Glu Ala Lys Asn Ile Lys Leu Gly Ala Gly Phe	
530 535 540	
caa gac gtt aac gca gaa gat aaa gta agc tgg aaa ggc acg att gac	1680
Gln Asp Val Asn Ala Glu Asp Lys Val Ser Trp Lys Gly Thr Ile Asp	
545 550 555 560	
ctg tct aaa caa gac aag ccg ttt gca cag tct cca caa tgt cag acg	1728
Leu Ser Lys Gln Asp Lys Pro Phe Ala Gln Ser Pro Gln Cys Gln Thr	
565 570 575	
cta atc aca gat ggc aca gtc agt gac ttt gct cac cta cca agc cac	1776
Leu Ile Thr Asp Gly Thr Val Ser Asp Phe Ala His Leu Pro Ser His	
580 585 590	
ttc gcg gaa gaa gtg tcg aag att gtt gct gag aaa ggc att cca aac	1824
Phe Ala Glu Glu Val Ser Lys Ile Val Ala Glu Lys Gly Ile Pro Asn	
595 600 605	
ttc caa gct tgg caa gat ggt ttg aaa tac agt gac ggc gaa aaa gcg	1872
Phe Gln Ala Trp Gln Asp Gly Leu Lys Tyr Ser Asp Gly Glu Lys Ala	
610 615 620	
ttc gct aca gaa aat act cgc gta aac ttc tgg gac gtt ctg tac tgg	1920

Phe	Ala	Thr	Glu	Asn	Thr	Arg	Val	Asn	Phe	Trp	Asp	Val	Leu	Tyr	Trp		
625					630				635						640		
ggc	ggt	act	tcc	tca	gtg	tac	gag	tgg	tct	aag	aaa	ggt	tac	gac	gtg		1968
Gly	Gly	Thr	Ser	Ser	Val	Tyr	Glu	Trp	Ser	Lys	Lys	Gly	Tyr	Asp	Val		
			645					650					655				
att	gtt	tct	aac	cca	gat	tac	gtg	tac	atg	gat	atg	cca	tac	gaa	gtt		2016
Ile	Val	Ser	Asn	Pro	Asp	Tyr	Val	Tyr	Met	Asp	Met	Pro	Tyr	Glu	Val		
			660					665					670				
gac	ccg	aaa	gag	cgt	ggt	tac	tac	tgg	gca	aca	cgt	gca	acg	gat	act		2064
Asp	Pro	Lys	Glu	Arg	Gly	Tyr	Tyr	Trp	Ala	Thr	Arg	Ala	Thr	Asp	Thr		
		675					680					685					
cgt	aag	atg	ttt	ggc	ttt	gca	cca	gag	aac	atg	cct	caa	aac	gca	gaa		2112
Arg	Lys	Met	Phe	Gly	Phe	Ala	Pro	Glu	Asn	Met	Pro	Gln	Asn	Ala	Glu		
	690					695					700						
act	tct	gta	gat	cgc	gat	ggc	aat	ggc	ttt	act	ggt	aaa	ggt	gaa	atc		2160
Thr	Ser	Val	Asp	Arg	Asp	Gly	Asn	Gly	Phe	Thr	Gly	Lys	Gly	Glu	Ile		
705					710				715					720			
gaa	gcg	aaa	cct	ttc	tac	ggt	cta	tct	gca	caa	ctt	tgg	tct	gag	aca		2208
Glu	Ala	Lys	Pro	Phe	Tyr	Gly	Leu	Ser	Ala	Gln	Leu	Trp	Ser	Glu	Thr		
				725					730					735			
gta	cgt	aac	gac	gag	caa	tac	gag	tac	atg	gta	ttc	cct	cgc	gtc	ctc		2256
Val	Arg	Asn	Asp	Glu	Gln	Tyr	Glu	Tyr	Met	Val	Phe	Pro	Arg	Val	Leu		
			740					745					750				
gct	gct	gct	cag	cgt	gca	tgg	cac	cgt	gct	gac	tgg	gaa	aac	gac	tac		2304
Ala	Ala	Ala	Gln	Arg	Ala	Trp	His	Arg	Ala	Asp	Trp	Glu	Asn	Asp	Tyr		
		755				760						765					
aaa	gtt	ggt	gtt	gag	tac	tcg	caa	aac	tct	aat	cta	gtt	gat	aaa	gca		2352
Lys	Val	Gly	Val	Glu	Tyr	Ser	Gln	Asn	Ser	Asn	Leu	Val	Asp	Lys	Ala		
	770					775					780						
tcg	cta	aac	caa	gac	tac	aac	cgc	ttt	gcg	aac	gta	ctt	ggt	caa	cgt		2400
Ser	Leu	Asn	Gln	Asp	Tyr	Asn	Arg	Phe	Ala	Asn	Val	Leu	Gly	Gln	Arg		
785					790					795				800			
gaa	ctg	gct	aag	cta	gaa	aaa	tca	ggt	att	gac	tac	cgc	cta	cca	gta		2448
Glu	Leu	Ala	Lys	Leu	Glu	Lys	Ser	Gly	Ile	Asp	Tyr	Arg	Leu	Pro	Val		
			805					810					815				
cca	ggt	gca	aaa	gta	gaa	gat	ggt	aag	cta	gca	atg	aac	gtt	cag	ttc		2496
Pro	Gly	Ala	Lys	Val	Glu	Asp	Gly	Lys	Leu	Ala	Met	Asn	Val	Gln	Phe		
			820				825						830				
cct	ggc	gta	acg	ctt	caa	tac	tct	ctg	gat	ggt	gag	aac	tgg	ttg	act		2544
Pro	Gly	Val	Thr	Leu	Gln	Tyr	Ser	Leu	Asp	Gly	Glu	Asn	Trp	Leu	Thr		
		835					840					845					
tat	gca	gac	aac	gct	cgt	cca	aat	gta	act	ggt	gaa	gtc	ttc	atc	cgc		2592
Tyr	Ala	Asp	Asn	Ala	Arg	Pro	Asn	Val	Thr	Gly	Glu	Val	Phe	Ile	Arg		

850

855

860

tcg gta tct gcg aca ggt gag aag gta agc cgt atc act agc gtg aaa 2640
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taa 2643
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<210> 19

<211> 880

<212> PRT

<213> Artificial Sequence

<220>

<223> dnaA/Chitobiase Fusion

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 Leu Asp Ile Gln Tyr Glu Val Leu Thr Asn His Gly Ala Asn Glu Gly
 35 40 45
 Leu Ala Cys Gln Asp Met Gly Ala Glu Trp Ala Ser Cys Asn Lys Val
 50 55 60
 Asn Met Thr Leu Val Asn Gln Gly Glu Ala Val Asp Ser Lys Asp Trp
 65 70 75 80
 Ala Ile Tyr Phe His Ser Ile Arg Leu Ile Leu Asp Val Asp Asn Glu
 85 90 95
 Gln Phe Lys Ile Ser Arg Val Thr Gly Asp Leu His Lys Leu Glu Pro
 100 105 110
 Thr Asp Lys Phe Asp Gly Phe Ala Ala Gly Glu Glu Val Val Leu Pro
 115 120 125
 Leu Val Gly Glu Tyr Trp Gln Leu Phe Glu Thr Asp Phe Met Pro Gly
 130 135 140
 Ala Phe Val Ser Ala Pro Asn Ala Glu Pro Lys Met Ile Ala Ser Leu
 145 150 155 160
 Asn Thr Glu Asp Val Ala Ser Phe Val Thr Gly Leu Glu Gly Asn Asn
 165 170 175
 Leu Lys Arg Thr Pro Asp Asp Asn Asn Val Phe Ala Asn Ala Val Ser
 180 185 190
 Arg Phe Glu Lys Asn Glu Asp Leu Ala Thr Gln Asp Val Ser Thr Thr
 195 200 205
 Leu Leu Pro Thr Pro Met His Val Glu Ala Gly Lys Gly Lys Val Asp
 210 215 220
 Ile Ala Asp Gly Ile Ala Leu Pro Lys Asp Ala Phe Asp Ala Thr Gln
 225 230 235 240
 Phe Ala Ala Ile Gln Asp Arg Ala Glu Val Val Gly Val Asp Val Arg
 245 250 255
 Gly Asp Leu Pro Val Ser Ile Thr Val Val Pro Ala Asp Phe Thr Gly
 260 265 270
 Glu Leu Ala Lys Ser Gly Ala Tyr Glu Met Ser Ile Lys Gly Asp Gly
 275 280 285
 Ile Val Ile Lys Ala Phe Asp Gln Ala Gly Ala Phe Tyr Ala Val Gln
 290 295 300
 Ser Ile Phe Gly Leu Val Asp Ser Gln Asn Ala Asp Ser Leu Pro Gln

305 310 315 320
 Leu Ser Ile Lys Asp Ala Pro Arg Phe Asp Tyr Arg Gly Val Met Val
 325 330 335
 Asp Val Ala Arg Asn Phe His Ser Lys Asp Ala Ile Leu Ala Thr Leu
 340 345 350
 Asp Gln Met Ala Ala Tyr Lys Met Asn Lys Leu His Leu His Leu Thr
 355 360 365
 Asp Asp Glu Gly Trp Arg Leu Glu Ile Pro Gly Leu Pro Glu Leu Thr
 370 375 380
 Glu Val Gly Ala Asn Arg Cys Phe Asp Thr Gln Glu Lys Ser Cys Leu
 385 390 395 400
 Leu Pro Gln Leu Gly Ser Gly Pro Thr Thr Asp Asn Phe Gly Ser Gly
 405 410 415
 Tyr Phe Ser Lys Ala Asp Tyr Val Glu Ile Leu Lys Tyr Ala Lys Ala
 420 425 430
 Arg Asn Ile Glu Val Ile Pro Glu Ile Asp Met Pro Ala His Ala Arg
 435 440 445
 Ala Ala Val Val Ser Met Glu Ala Arg Tyr Asp Arg Leu Met Glu Glu
 450 455 460
 Gly Lys Glu Ala Glu Ala Asn Glu Tyr Arg Leu Met Asp Pro Gln Asp
 465 470 475 480
 Thr Ser Asn Val Thr Thr Val Gln Phe Tyr Asn Lys Gln Ser Phe Ile
 485 490 495
 Asn Pro Cys Met Glu Ser Ser Thr Arg Phe Val Asp Lys Val Ile Ser
 500 505 510
 Glu Val Ala Ala Met His Gln Glu Ala Gly Ala Pro Leu Thr Thr Trp
 515 520 525
 His Phe Gly Gly Asp Glu Ala Lys Asn Ile Lys Leu Gly Ala Gly Phe
 530 535 540
 Gln Asp Val Asn Ala Glu Asp Lys Val Ser Trp Lys Gly Thr Ile Asp
 545 550 555 560
 Leu Ser Lys Gln Asp Lys Pro Phe Ala Gln Ser Pro Gln Cys Gln Thr
 565 570 575
 Leu Ile Thr Asp Gly Thr Val Ser Asp Phe Ala His Leu Pro Ser His
 580 585 590
 Phe Ala Glu Glu Val Ser Lys Ile Val Ala Glu Lys Gly Ile Pro Asn
 595 600 605
 Phe Gln Ala Trp Gln Asp Gly Leu Lys Tyr Ser Asp Gly Glu Lys Ala
 610 615 620
 Phe Ala Thr Glu Asn Thr Arg Val Asn Phe Trp Asp Val Leu Tyr Trp
 625 630 635 640
 Gly Gly Thr Ser Ser Val Tyr Glu Trp Ser Lys Lys Gly Tyr Asp Val
 645 650 655
 Ile Val Ser Asn Pro Asp Tyr Val Tyr Met Asp Met Pro Tyr Glu Val
 660 665 670
 Asp Pro Lys Glu Arg Gly Tyr Tyr Trp Ala Thr Arg Ala Thr Asp Thr
 675 680 685
 Arg Lys Met Phe Gly Phe Ala Pro Glu Asn Met Pro Gln Asn Ala Glu
 690 695 700
 Thr Ser Val Asp Arg Asp Gly Asn Gly Phe Thr Gly Lys Gly Glu Ile
 705 710 715 720
 Glu Ala Lys Pro Phe Tyr Gly Leu Ser Ala Gln Leu Trp Ser Glu Thr
 725 730 735
 Val Arg Asn Asp Glu Gln Tyr Glu Tyr Met Val Phe Pro Arg Val Leu
 740 745 750
 Ala Ala Ala Gln Arg Ala Trp His Arg Ala Asp Trp Glu Asn Asp Tyr
 755 760 765

Lys Val Gly Val Glu Tyr Ser Gln Asn Ser Asn Leu Val Asp Lys Ala
 770 775 780
 Ser Leu Asn Gln Asp Tyr Asn Arg Phe Ala Asn Val Leu Gly Gln Arg
 785 790 795 800
 Glu Leu Ala Lys Leu Glu Lys Ser Gly Ile Asp Tyr Arg Leu Pro Val
 805 810 815
 Pro Gly Ala Lys Val Glu Asp Gly Lys Leu Ala Met Asn Val Gln Phe
 820 825 830
 Pro Gly Val Thr Leu Gln Tyr Ser Leu Asp Gly Glu Asn Trp Leu Thr
 835 840 845
 Tyr Ala Asp Asn Ala Arg Pro Asn Val Thr Gly Glu Val Phe Ile Arg
 850 855 860
 Ser Val Ser Ala Thr Gly Glu Lys Val Ser Arg Ile Thr Ser Val Lys
 865 870 875 880

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 Concluded